



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 26, 2024 – 02:08 AM EDT

PDB ID : 6RTI
Title : X-ray structure of human glutamate carboxypeptidase II (GCPII) in complex with aptamer A9g
Authors : Motlova, L.; Kolenko, P.; Barinka, C.
Deposited on : 2019-05-24
Resolution : 2.20 Å (reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.37.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

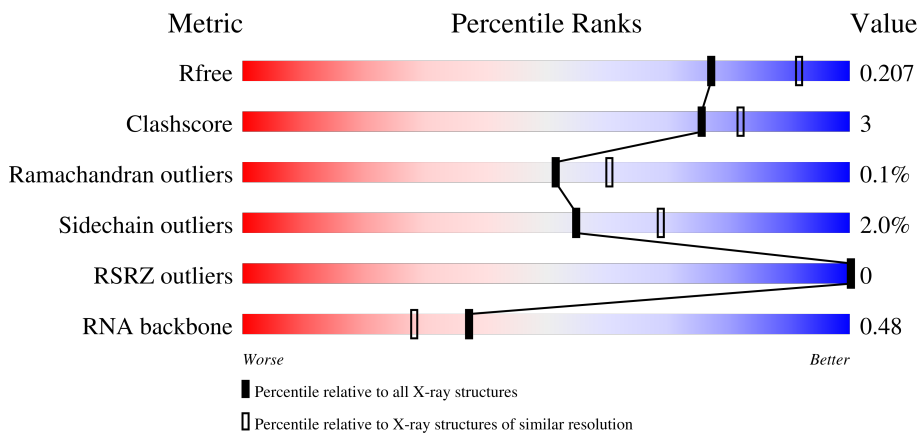
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


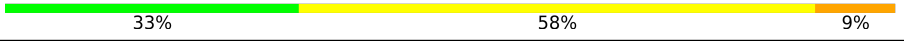
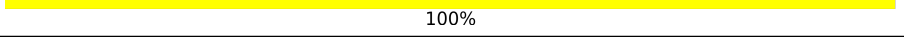

The reported resolution of this entry is 2.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)
RNA backbone	3102	1032 (2.60-1.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	707	 91% 7% ..
2	X	43	 33% 58% 9%
3	B	3	 100%
3	D	3	 33% 67%

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Mol	Chain	Length	Quality of chain
3	G	3	 33% 67%
4	C	2	 100%
4	E	2	 50% 50%
4	H	2	 100%
5	F	4	 25% 75%

2 Entry composition [i](#)

There are 12 unique types of molecules in this entry. The entry contains 7271 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

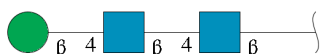
- Molecule 1 is a protein called Glutamate carboxypeptidase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	693	5575	3583	933	1040	19	0	15	0

- Molecule 2 is a RNA chain called Aptamer A9g, RNA (43-MER).

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	F	N	O	P			
2	X	43	974	438	22	176	293	45	0	3	0

- Molecule 3 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



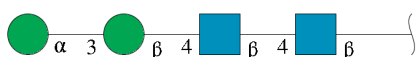
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	B	3	39	22	2	15	0	0	0
3	D	3	39	22	2	15	0	0	0
3	G	3	39	22	2	15	0	0	0

- Molecule 4 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	C	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	E	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	H	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 5 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	F	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	2	Total	Zn	0	0
			2	2		

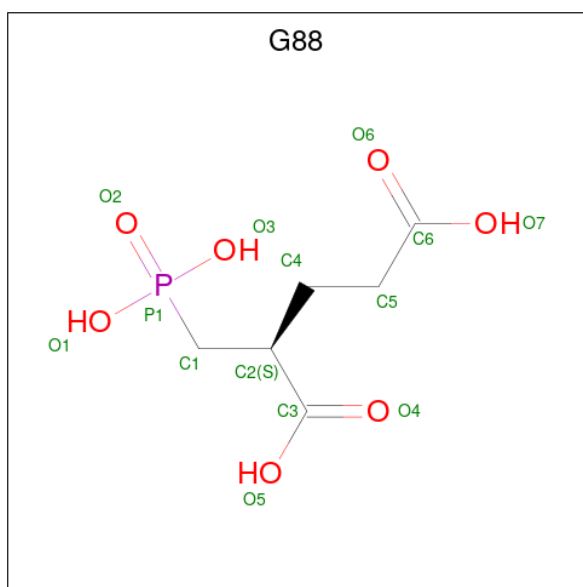
- Molecule 7 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Cl	0	0
			1	1		

- Molecule 8 is CALCIUM ION (three-letter code: CA) (formula: Ca).

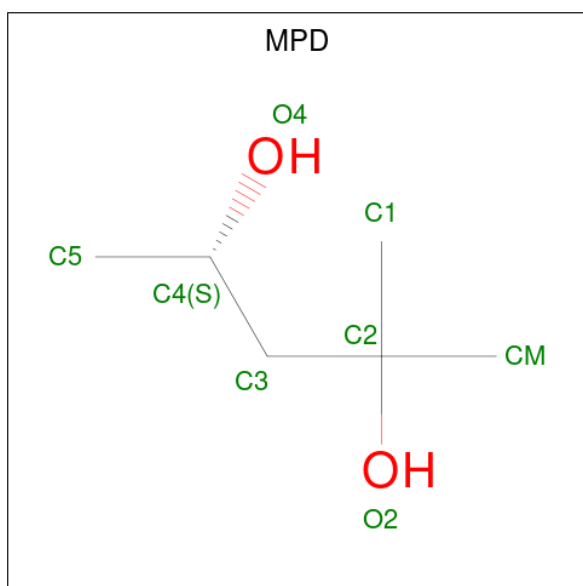
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	1	Total	Ca	0	0
			1	1		

- Molecule 9 is (2S)-2-(PHOSPHONOMETHYL)PENTANEDIOIC ACID (three-letter code: G88) (formula: C₆H₁₁O₇P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	A	1	Total	C	O	P	0	0
			14	6	7	1		

- Molecule 10 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: $C_6H_{14}O_2$).



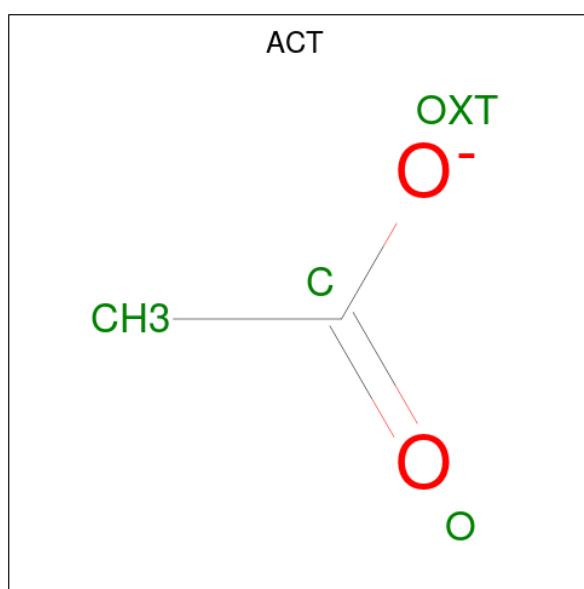
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			8	6	2		
10	A	1	Total	C	O	0	0
			8	6	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			8	6	2		
10	X	1	Total	C	O	0	0
			8	6	2		
10	X	1	Total	C	O	0	0
			8	6	2		
10	X	1	Total	C	O	0	0
			8	6	2		

- Molecule 11 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	A	1	Total	C	O	0	0
			4	2	2		

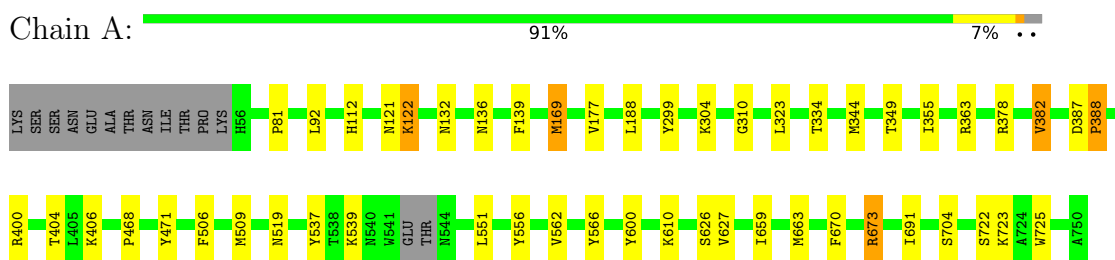
- Molecule 12 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	321	Total	O	0	1
			321	321		
12	X	80	Total	O	0	1
			80	80		

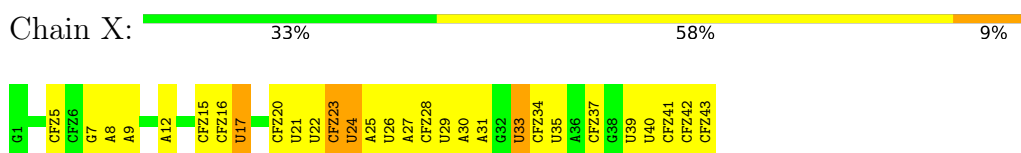
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

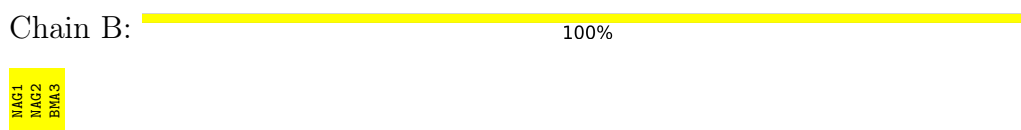
- Molecule 1: Glutamate carboxypeptidase 2



- Molecule 2: Aptamer A9g, RNA (43-MER)



- Molecule 3: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 3: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose




- Molecule 3: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



MAG1
MAG2
BMA3

- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C:  100%


MAG1
MAG2

- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:  50%

MAG1
MAG2

- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H:  100%

MAG1
MAG2

- Molecule 5: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:  25%

MAG1
MAG2
BMA3
MAM4

4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	121.10Å 121.10Å 216.27Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	105.66 – 2.20 105.66 – 2.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (105.66-2.20) 100.0 (105.66-2.20)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.72 (at 2.20Å)	Xtrriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.192 , 0.217 0.202 , 0.207	Depositor DCC
R_{free} test set	4036 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	36.2	Xtrriage
Anisotropy	0.507	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 39.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7271	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.86% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MAN, MPD, ZN, G88, BMA, CA, ACT, UFT, CFZ, CL, NAG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.65	0/5787	0.77	1/7840 (0.0%)
2	X	0.39	0/603	0.74	0/938
All	All	0.63	0/6390	0.76	1/8778 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	673	ARG	CG-CD-NE	-5.24	100.80	111.80

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5575	0	5436	29	0
2	X	974	0	476	12	0
3	B	39	0	34	0	0
3	D	39	0	34	0	0
3	G	39	0	34	0	0
4	C	28	0	25	0	0
4	E	28	0	25	0	0
4	H	28	0	25	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	F	50	0	43	0	0
6	A	2	0	0	0	0
7	A	1	0	0	0	0
8	A	1	0	0	0	0
9	A	14	0	8	0	0
10	A	24	0	42	0	0
10	X	24	0	42	0	0
11	A	4	0	3	0	0
12	A	321	0	0	1	0
12	X	80	0	0	1	0
All	All	7271	0	6227	40	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 40 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X:9[A]:A:N6	12:X:201:HOH:O	1.93	1.02
2:X:7[B]:G:H5''	2:X:8[B]:A:H5'	1.49	0.93
1:A:122[A]:LYS:HE3	1:A:122[A]:LYS:H	1.34	0.91
1:A:122[A]:LYS:H	1:A:122[A]:LYS:CE	2.05	0.69
2:X:7[B]:G:H5'	2:X:8[B]:A:H8	1.59	0.67

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	704/707 (100%)	683 (97%)	20 (3%)	1 (0%)	51 60

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	382	VAL

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	605/603 (100%)	592 (98%)	13 (2%)	53 67

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	537	TYR
1	A	539	LYS
1	A	723	LYS
1	A	626	SER
1	A	722	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	X	17/43 (39%)	4 (23%)	0

All (4) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	X	12	A
2	X	25	A
2	X	27	A
2	X	30	A

There are no RNA pucker outliers to report.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

22 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	UFT	X	24	2	18,21,22	1.28	2 (11%)	26,30,33	2.10	6 (23%)
2	UFT	X	39	2	18,21,22	1.49	3 (16%)	26,30,33	1.83	5 (19%)
2	CFZ	X	43	2	18,21,22	0.79	0	26,30,33	0.93	1 (3%)
2	UFT	X	17	2	18,21,22	1.48	5 (27%)	26,30,33	1.87	6 (23%)
2	CFZ	X	20	2	18,21,22	1.03	1 (5%)	26,30,33	1.15	1 (3%)
2	UFT	X	22	2	18,21,22	1.22	2 (11%)	26,30,33	1.87	6 (23%)
2	CFZ	X	41	2	18,21,22	1.03	0	26,30,33	1.15	2 (7%)
2	UFT	X	33	2	18,21,22	1.55	4 (22%)	26,30,33	1.67	6 (23%)
2	UFT	X	40	2	18,21,22	1.32	1 (5%)	26,30,33	1.94	6 (23%)
2	CFZ	X	23	2	18,21,22	0.89	0	26,30,33	1.07	1 (3%)
2	CFZ	X	37	2	18,21,22	0.94	1 (5%)	26,30,33	0.96	1 (3%)
2	CFZ	X	28	2	18,21,22	0.90	0	26,30,33	1.00	1 (3%)
2	CFZ	X	16	2	18,21,22	1.12	2 (11%)	26,30,33	0.97	1 (3%)
2	CFZ	X	42	2	18,21,22	0.94	0	26,30,33	1.08	1 (3%)
2	UFT	X	26	2	18,21,22	1.42	3 (16%)	26,30,33	1.76	6 (23%)
2	UFT	X	29	2	18,21,22	1.36	2 (11%)	26,30,33	1.86	6 (23%)
2	CFZ	X	5	2	18,21,22	0.98	1 (5%)	26,30,33	1.02	1 (3%)
2	CFZ	X	34	2	18,21,22	1.27	1 (5%)	26,30,33	0.84	0
2	UFT	X	35	2	18,21,22	1.46	4 (22%)	26,30,33	1.62	4 (15%)
2	CFZ	X	6	2	18,21,22	0.92	0	26,30,33	0.87	0
2	CFZ	X	15	2	18,21,22	1.08	0	26,30,33	1.04	1 (3%)
2	UFT	X	21	2	18,21,22	1.41	3 (16%)	26,30,33	1.71	5 (19%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	UFT	X	24	2	-	0/7/25/26	0/2/2/2
2	UFT	X	39	2	-	0/7/25/26	0/2/2/2
2	CFZ	X	43	2	-	0/7/25/26	0/2/2/2
2	UFT	X	17	2	-	0/7/25/26	0/2/2/2
2	CFZ	X	20	2	-	0/7/25/26	0/2/2/2
2	UFT	X	22	2	-	0/7/25/26	0/2/2/2
2	CFZ	X	41	2	-	0/7/25/26	0/2/2/2
2	UFT	X	33	2	-	0/7/25/26	0/2/2/2
2	UFT	X	40	2	-	0/7/25/26	0/2/2/2
2	CFZ	X	23	2	-	0/7/25/26	0/2/2/2
2	CFZ	X	37	2	-	0/7/25/26	0/2/2/2
2	CFZ	X	28	2	-	2/7/25/26	0/2/2/2
2	CFZ	X	16	2	-	0/7/25/26	0/2/2/2
2	CFZ	X	42	2	-	0/7/25/26	0/2/2/2
2	UFT	X	26	2	-	6/7/25/26	0/2/2/2
2	UFT	X	29	2	-	0/7/25/26	0/2/2/2
2	CFZ	X	5	2	-	0/7/25/26	0/2/2/2
2	CFZ	X	34	2	-	0/7/25/26	0/2/2/2
2	UFT	X	35	2	-	0/7/25/26	0/2/2/2
2	CFZ	X	6	2	-	0/7/25/26	0/2/2/2
2	CFZ	X	15	2	-	1/7/25/26	0/2/2/2
2	UFT	X	21	2	-	0/7/25/26	0/2/2/2

The worst 5 of 35 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	X	39	UFT	C2-N1	3.03	1.43	1.38
2	X	24	UFT	C4-N3	-2.96	1.33	1.38
2	X	34	CFZ	C2'-C1'	-2.93	1.49	1.53
2	X	26	UFT	C2-N1	2.88	1.43	1.38
2	X	17	UFT	C4-N3	-2.85	1.33	1.38

The worst 5 of 67 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	X	24	UFT	C2'-C1'-N1	-5.27	106.14	114.20
2	X	40	UFT	C4-N3-C2	-4.98	120.02	126.58
2	X	40	UFT	N3-C2-N1	4.93	121.44	114.89
2	X	22	UFT	N3-C2-N1	4.64	121.05	114.89
2	X	39	UFT	C4-N3-C2	-4.62	120.49	126.58

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	X	26	UFT	C2'-C1'-N1-C6
2	X	26	UFT	C2'-C1'-N1-C2
2	X	26	UFT	C3'-C4'-C5'-O5'
2	X	26	UFT	O4'-C4'-C5'-O5'
2	X	26	UFT	O4'-C1'-N1-C6

There are no ring outliers.

4 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	X	24	UFT	1	0
2	X	17	UFT	1	0
2	X	33	UFT	1	0
2	X	23	CFZ	1	0

5.5 Carbohydrates [i](#)

19 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	B	1	1,3	14,14,15	0.44	0	17,19,21	1.17	1 (5%)
3	NAG	B	2	3	14,14,15	0.37	0	17,19,21	1.71	4 (23%)
3	BMA	B	3	3	11,11,12	0.36	0	15,15,17	1.25	2 (13%)
4	NAG	C	1	4,1	14,14,15	0.49	0	17,19,21	1.22	2 (11%)
4	NAG	C	2	4	14,14,15	0.36	0	17,19,21	1.52	2 (11%)
3	NAG	D	1	1,3	14,14,15	0.47	0	17,19,21	1.15	3 (17%)
3	NAG	D	2	3	14,14,15	0.33	0	17,19,21	1.05	0
3	BMA	D	3	3	11,11,12	0.52	0	15,15,17	2.13	3 (20%)
4	NAG	E	1	4,1	14,14,15	0.67	0	17,19,21	1.01	0
4	NAG	E	2	4	14,14,15	0.56	0	17,19,21	1.49	2 (11%)
5	NAG	F	1	1,5	14,14,15	0.40	0	17,19,21	0.95	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	F	2	5	14,14,15	0.36	0	17,19,21	0.65	0
5	BMA	F	3	5	11,11,12	0.36	0	15,15,17	0.94	1 (6%)
5	MAN	F	4	5	11,11,12	0.60	0	15,15,17	2.32	5 (33%)
3	NAG	G	1	1,3	14,14,15	0.66	0	17,19,21	0.86	0
3	NAG	G	2	3	14,14,15	0.38	0	17,19,21	1.47	3 (17%)
3	BMA	G	3	3	11,11,12	0.60	0	15,15,17	1.48	3 (20%)
4	NAG	H	1	4,1	14,14,15	0.37	0	17,19,21	1.13	1 (5%)
4	NAG	H	2	4	14,14,15	0.47	0	17,19,21	1.49	2 (11%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	B	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	B	2	3	-	0/6/23/26	0/1/1/1
3	BMA	B	3	3	-	2/2/19/22	0/1/1/1
4	NAG	C	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	C	2	4	-	1/6/23/26	0/1/1/1
3	NAG	D	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	D	2	3	-	0/6/23/26	0/1/1/1
3	BMA	D	3	3	-	0/2/19/22	0/1/1/1
4	NAG	E	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	E	2	4	-	2/6/23/26	0/1/1/1
5	NAG	F	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	F	2	5	-	0/6/23/26	0/1/1/1
5	BMA	F	3	5	-	0/2/19/22	0/1/1/1
5	MAN	F	4	5	-	2/2/19/22	0/1/1/1
3	NAG	G	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	G	2	3	-	0/6/23/26	0/1/1/1
3	BMA	G	3	3	-	1/2/19/22	0/1/1/1
4	NAG	H	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	H	2	4	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	4	MAN	C1-C2-C3	5.90	116.92	109.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	3	BMA	O5-C1-C2	5.46	119.20	110.77
4	H	2	NAG	O5-C1-C2	4.74	118.77	111.29
4	C	2	NAG	C1-O5-C5	4.44	118.20	112.19
3	B	2	NAG	O5-C1-C2	4.26	118.01	111.29

There are no chirality outliers.

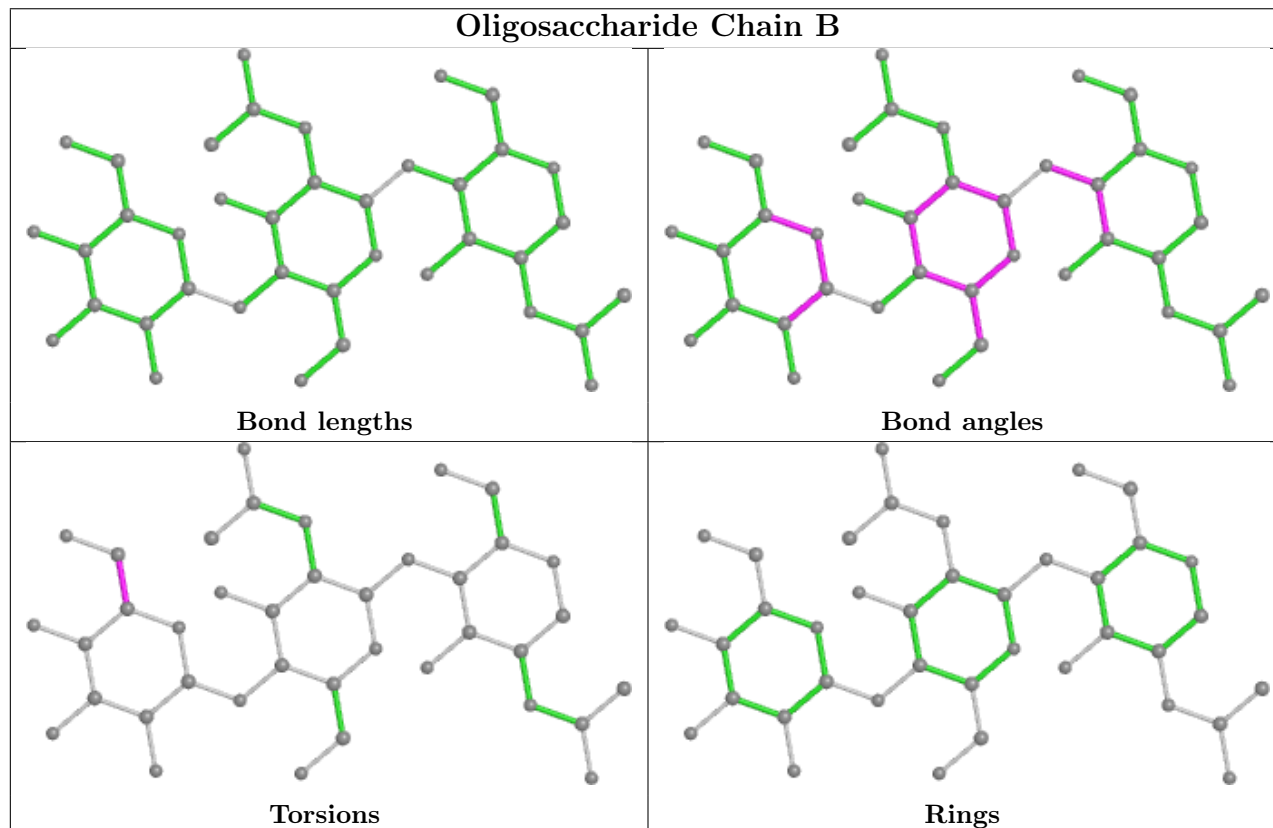
5 of 10 torsion outliers are listed below:

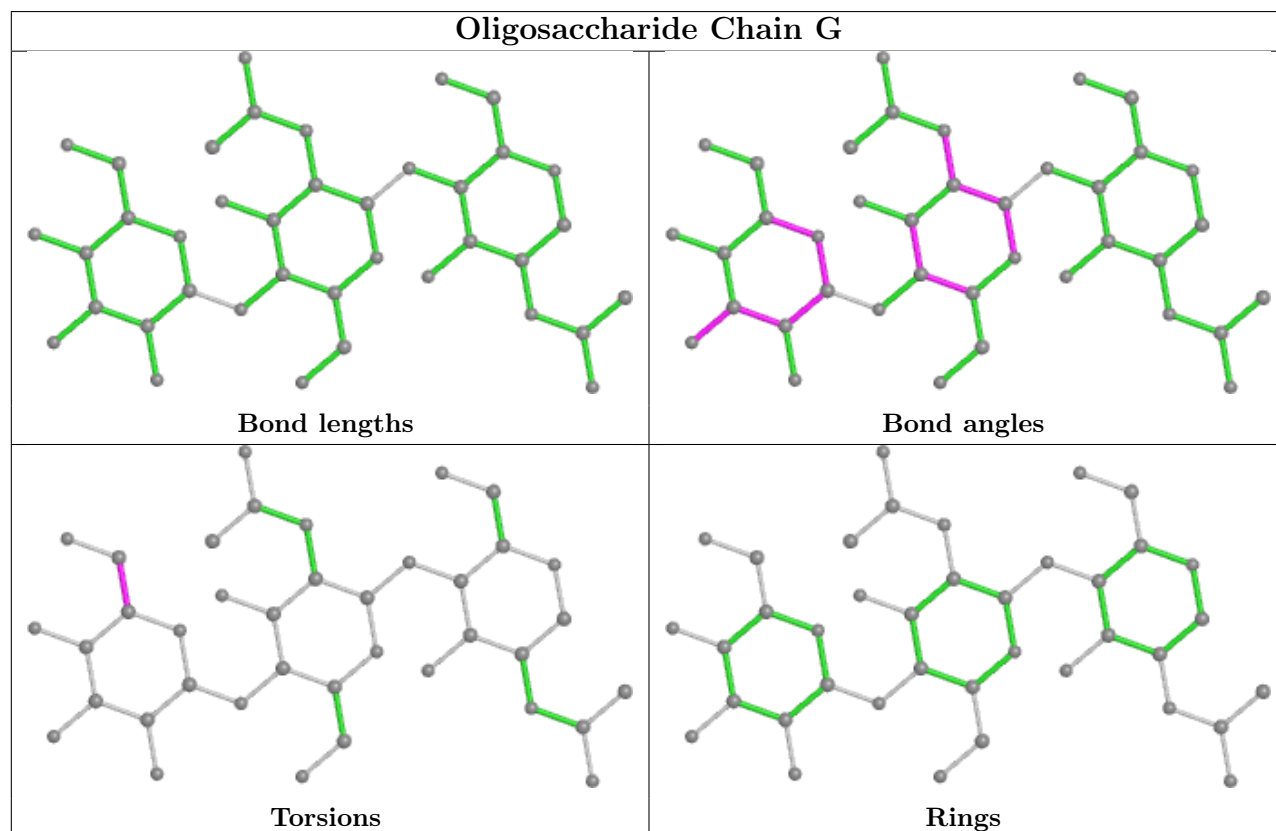
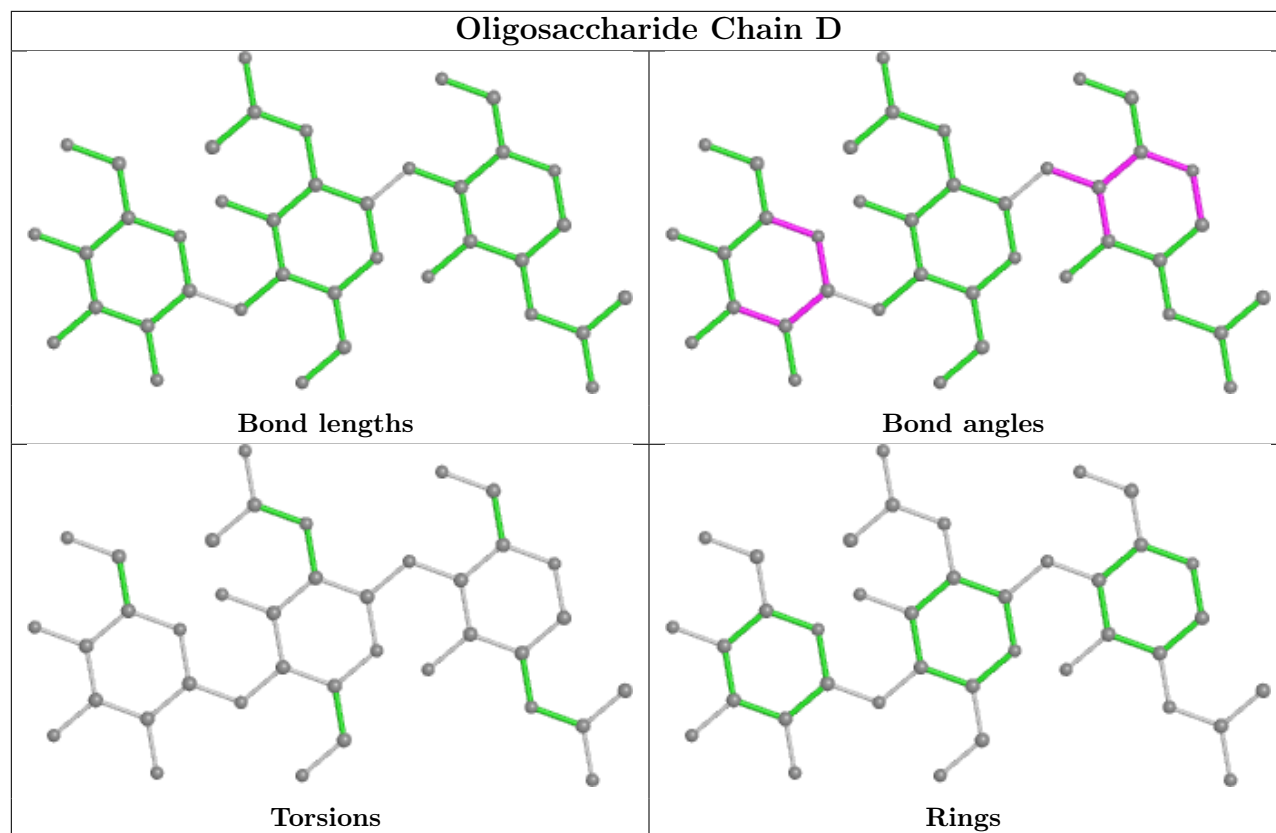
Mol	Chain	Res	Type	Atoms
5	F	4	MAN	O5-C5-C6-O6
4	C	1	NAG	C8-C7-N2-C2
4	C	1	NAG	O7-C7-N2-C2
4	E	2	NAG	O5-C5-C6-O6
5	F	4	MAN	C4-C5-C6-O6

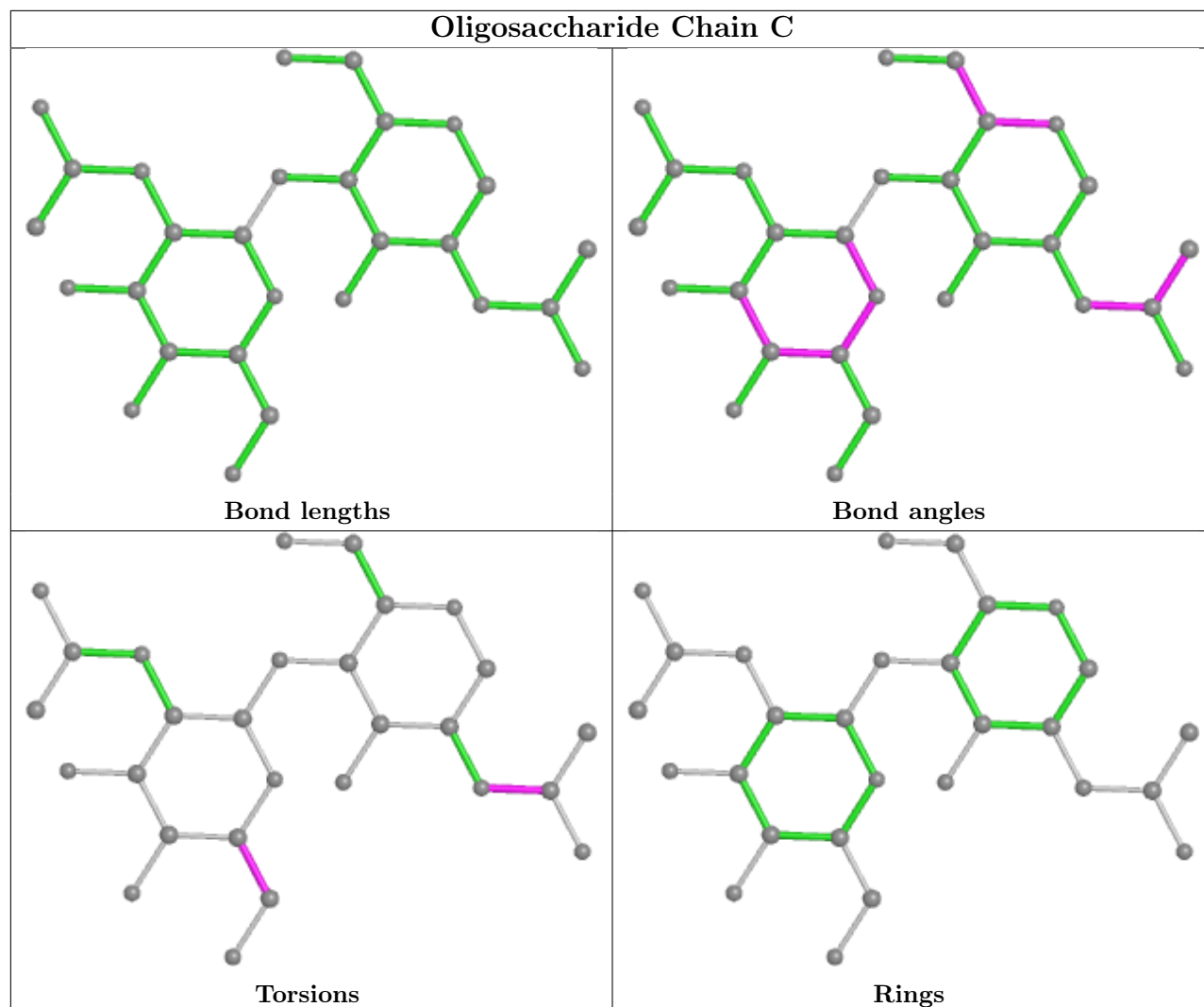
There are no ring outliers.

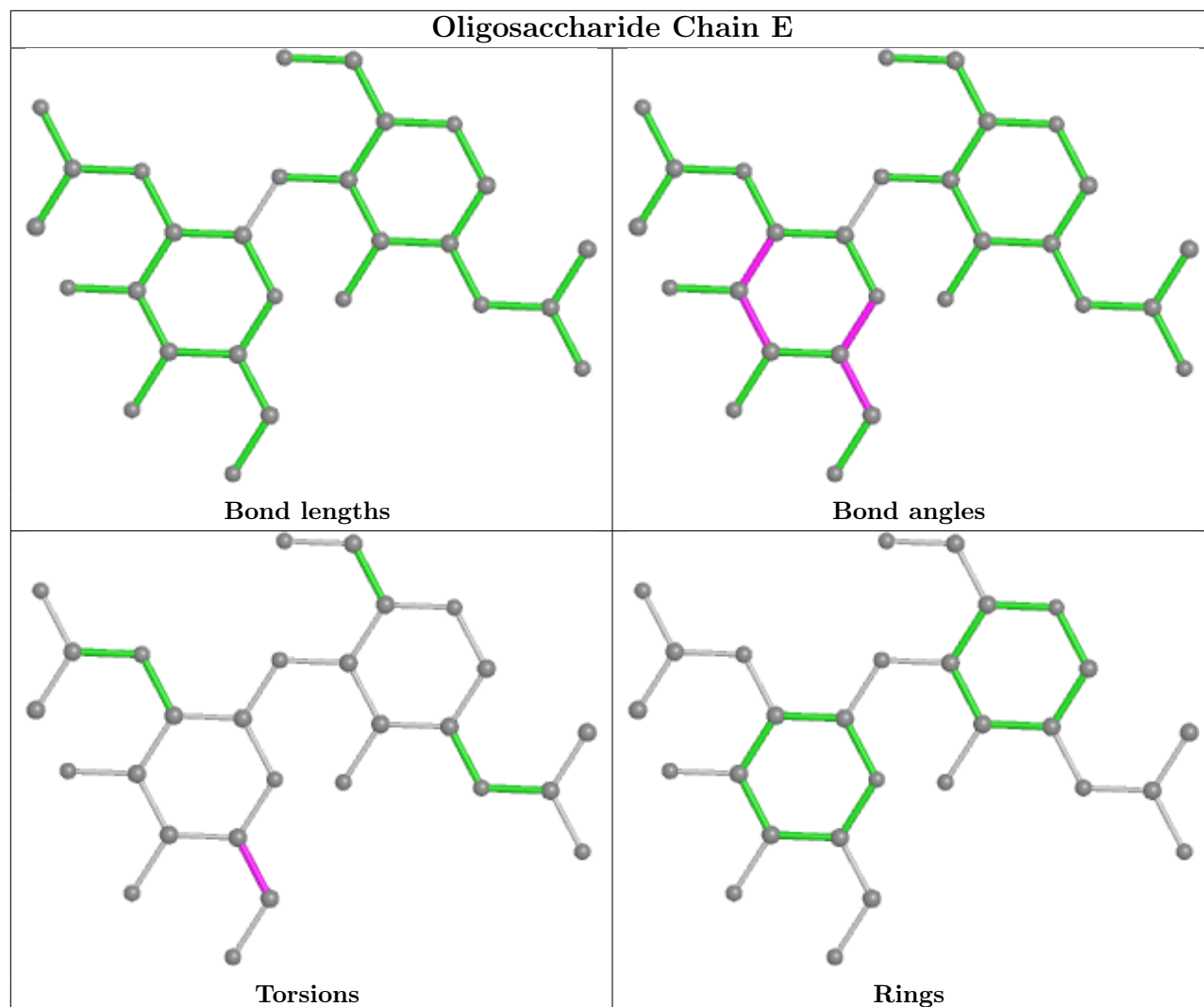
No monomer is involved in short contacts.

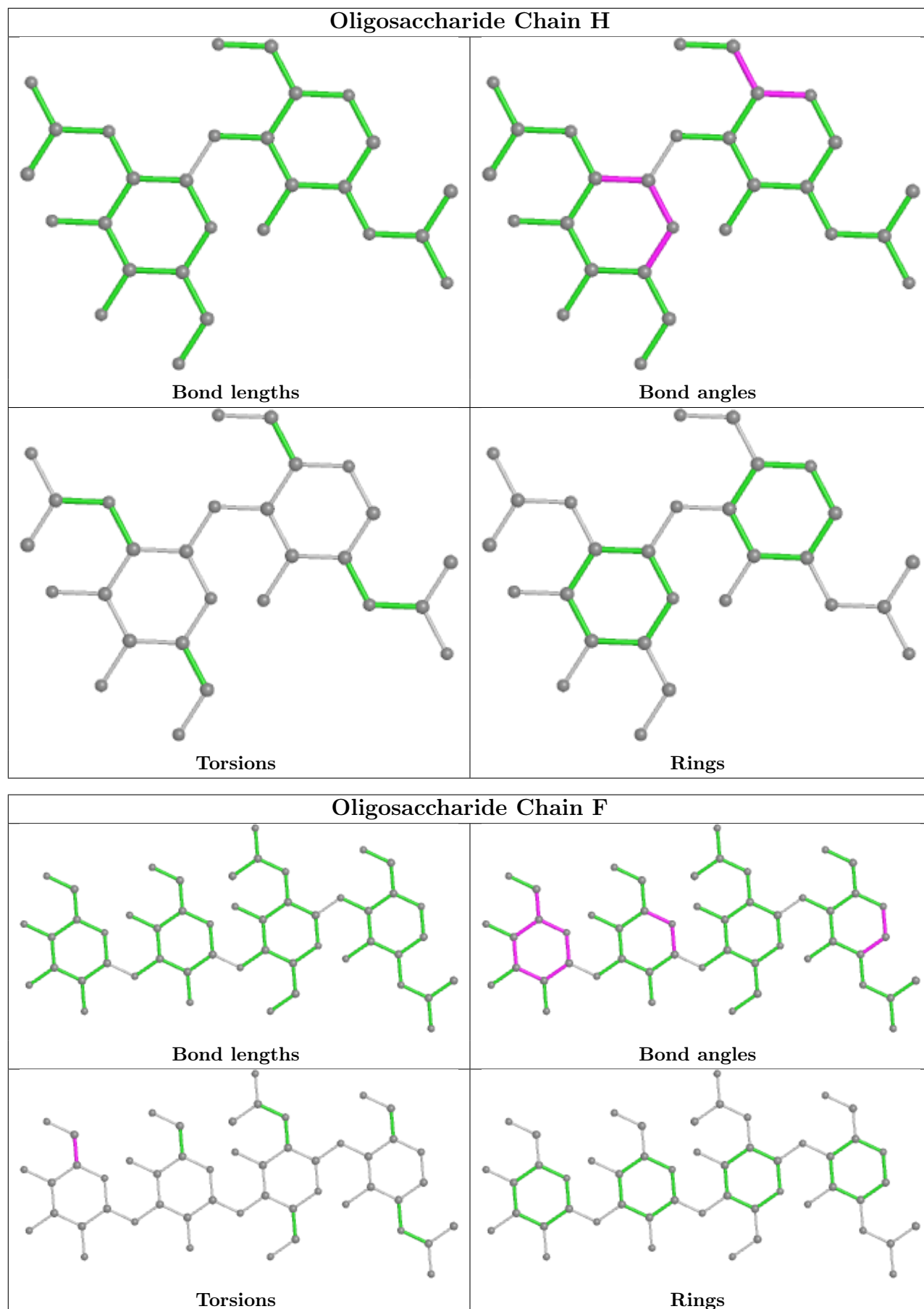
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











5.6 Ligand geometry

Of 12 ligands modelled in this entry, 4 are monoatomic - leaving 8 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
10	MPD	X	103	-	7,7,7	0.14	0	9,10,10	0.44	0
11	ACT	A	928	-	3,3,3	0.92	0	3,3,3	0.93	0
10	MPD	A	927	-	7,7,7	0.24	0	9,10,10	0.72	0
10	MPD	X	101	-	7,7,7	0.19	0	9,10,10	0.40	0
10	MPD	X	102	-	7,7,7	0.25	0	9,10,10	0.39	0
10	MPD	A	925	-	7,7,7	0.16	0	9,10,10	0.46	0
10	MPD	A	926	-	7,7,7	0.20	0	9,10,10	0.74	0
9	G88	A	905	6	12,13,13	1.58	2 (16%)	17,18,18	2.03	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
10	MPD	X	103	-	-	1/5/5/5	-
10	MPD	A	927	-	-	0/5/5/5	-
10	MPD	X	101	-	-	2/5/5/5	-
10	MPD	X	102	-	-	0/5/5/5	-
10	MPD	A	925	-	-	0/5/5/5	-
10	MPD	A	926	-	-	1/5/5/5	-
9	G88	A	905	6	-	3/14/14/14	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	905	G88	P1-O2	-3.69	1.42	1.50
9	A	905	G88	P1-O3	-2.16	1.50	1.54

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
9	A	905	G88	O2-P1-C1	-6.74	99.06	111.54

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	A	926	MPD	C2-C3-C4-O4
9	A	905	G88	C2-C1-P1-O3
9	A	905	G88	C4-C5-C6-O7
9	A	905	G88	C4-C5-C6-O6
10	X	101	MPD	C2-C3-C4-C5

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled '#RSRZ > 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q < 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	693/707 (98%)	-0.16	0 100 100	28, 41, 69, 100	1 (0%)
2	X	21/43 (48%)	-0.45	0 100 100	40, 55, 66, 81	0
All	All	714/750 (95%)	-0.17	0 100 100	28, 41, 69, 100	1 (0%)

There are no RSRZ outliers to report.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	CFZ	X	20	20/21	0.94	0.13	48,67,75,76	0
2	UFT	X	26	20/21	0.94	0.13	47,53,84,92	0
2	CFZ	X	42	20/21	0.94	0.10	54,64,71,74	0
2	UFT	X	40	20/21	0.96	0.11	43,50,57,65	0
2	CFZ	X	5	20/21	0.96	0.09	51,58,64,73	0
2	CFZ	X	37	20/21	0.97	0.09	56,59,62,63	0
2	UFT	X	39	20/21	0.97	0.09	45,50,58,60	0
2	UFT	X	21	20/21	0.97	0.11	40,52,56,58	0
2	CFZ	X	41	20/21	0.97	0.09	49,57,65,72	0
2	CFZ	X	6	20/21	0.97	0.09	50,59,64,67	0
2	CFZ	X	43	20/21	0.97	0.09	49,60,66,70	0
2	UFT	X	35	20/21	0.98	0.10	44,54,57,58	0
2	UFT	X	17	20/21	0.98	0.12	35,37,40,42	0
2	UFT	X	22	20/21	0.98	0.10	37,42,44,46	0
2	CFZ	X	23	20/21	0.98	0.11	40,42,46,47	0
2	UFT	X	24	20/21	0.98	0.12	41,45,48,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	CFZ	X	15	20/21	0.98	0.11	36,43,46,47	0
2	CFZ	X	28	20/21	0.98	0.11	37,38,43,44	0
2	CFZ	X	34	20/21	0.99	0.11	39,42,44,48	0
2	CFZ	X	16	20/21	0.99	0.12	38,41,45,45	0
2	UFT	X	29	20/21	0.99	0.13	36,39,47,48	0
2	UFT	X	33	20/21	0.99	0.12	39,42,44,45	0

6.3 Carbohydrates [\(i\)](#)

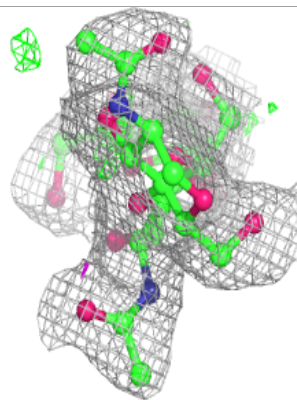
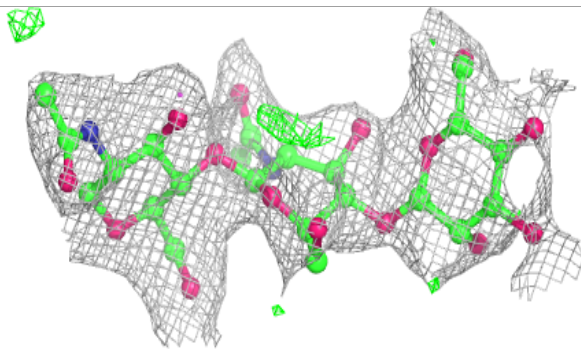
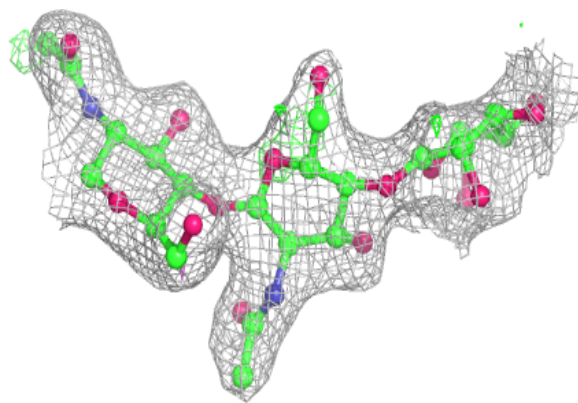
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	BMA	F	3	11/12	0.37	0.18	84,107,112,114	0
3	BMA	G	3	11/12	0.43	0.29	95,108,116,116	0
3	BMA	D	3	11/12	0.59	0.15	113,120,129,130	0
5	MAN	F	4	11/12	0.63	0.29	115,123,125,128	0
4	NAG	H	2	14/15	0.70	0.19	115,127,131,132	0
3	BMA	B	3	11/12	0.74	0.15	113,123,127,127	0
4	NAG	H	1	14/15	0.82	0.11	77,90,96,113	0
4	NAG	E	2	14/15	0.82	0.20	80,86,90,91	0
4	NAG	C	1	14/15	0.83	0.13	67,97,114,119	0
4	NAG	C	2	14/15	0.85	0.18	103,120,125,127	0
3	NAG	D	1	14/15	0.86	0.09	55,65,74,78	0
3	NAG	G	2	14/15	0.86	0.17	68,75,84,107	0
3	NAG	B	2	14/15	0.87	0.15	64,92,103,111	0
3	NAG	D	2	14/15	0.92	0.11	77,89,100,113	0
5	NAG	F	2	14/15	0.93	0.17	78,84,88,98	0
4	NAG	E	1	14/15	0.94	0.09	38,56,67,71	0
5	NAG	F	1	14/15	0.95	0.15	53,58,67,73	0
3	NAG	G	1	14/15	0.96	0.11	32,38,51,54	0
3	NAG	B	1	14/15	0.97	0.10	46,55,62,66	0

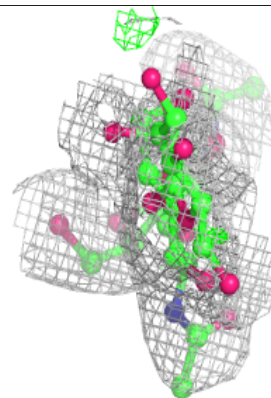
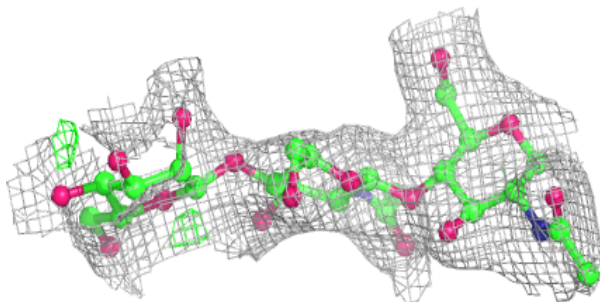
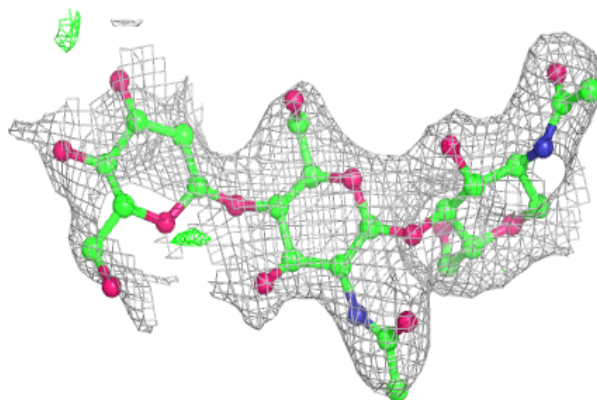
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

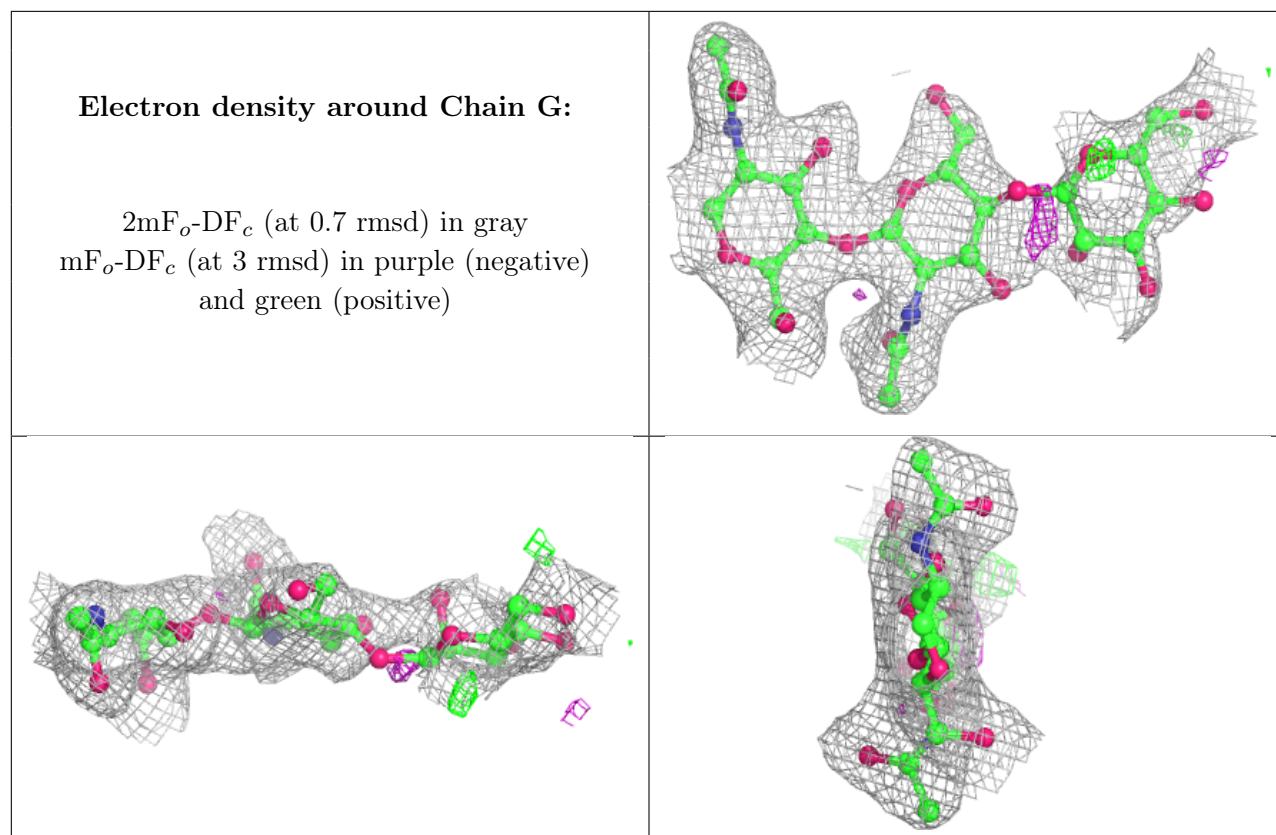
Electron density around Chain B:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around Chain D:**

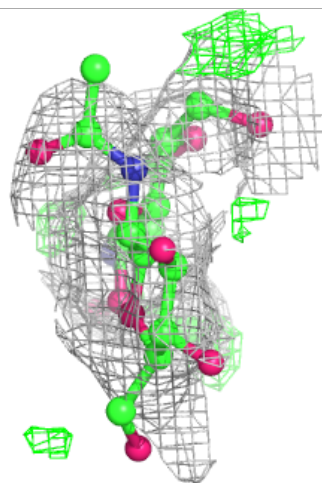
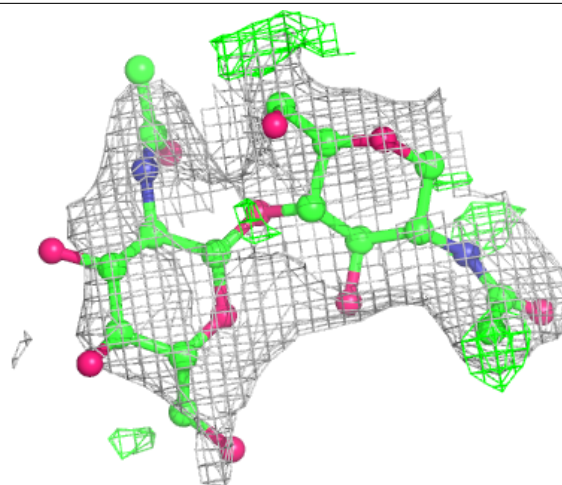
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





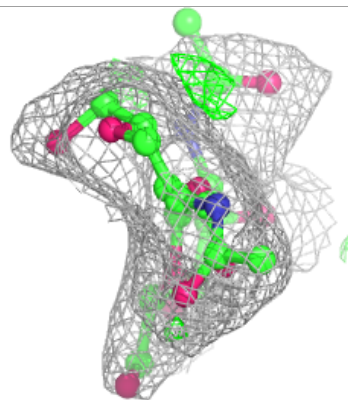
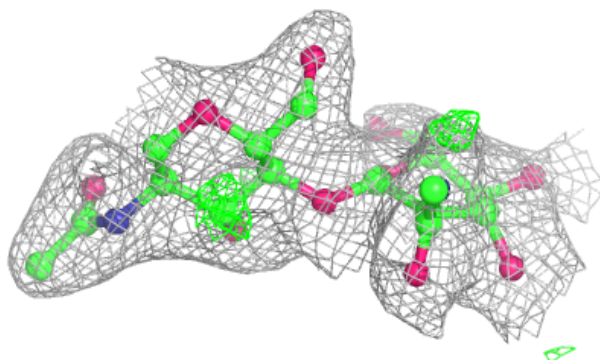
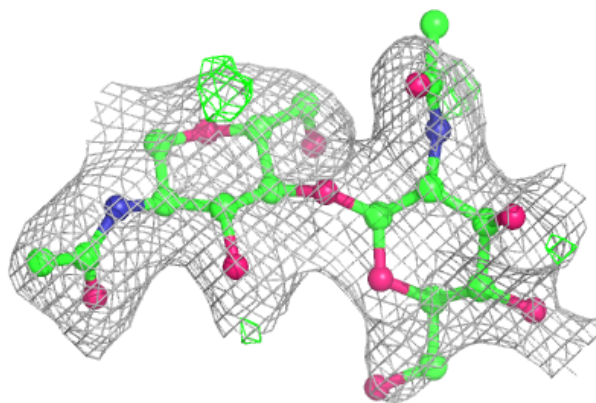
Electron density around Chain C:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

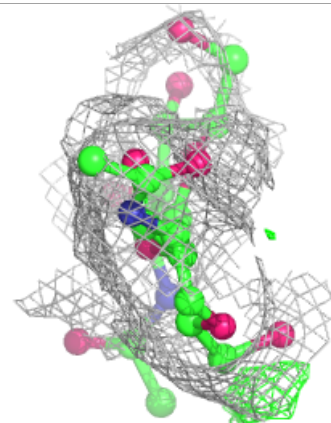
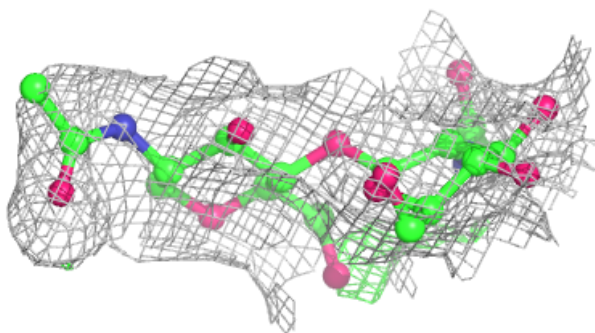
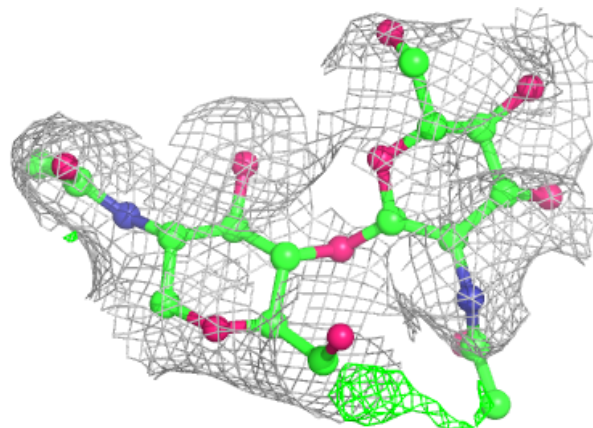


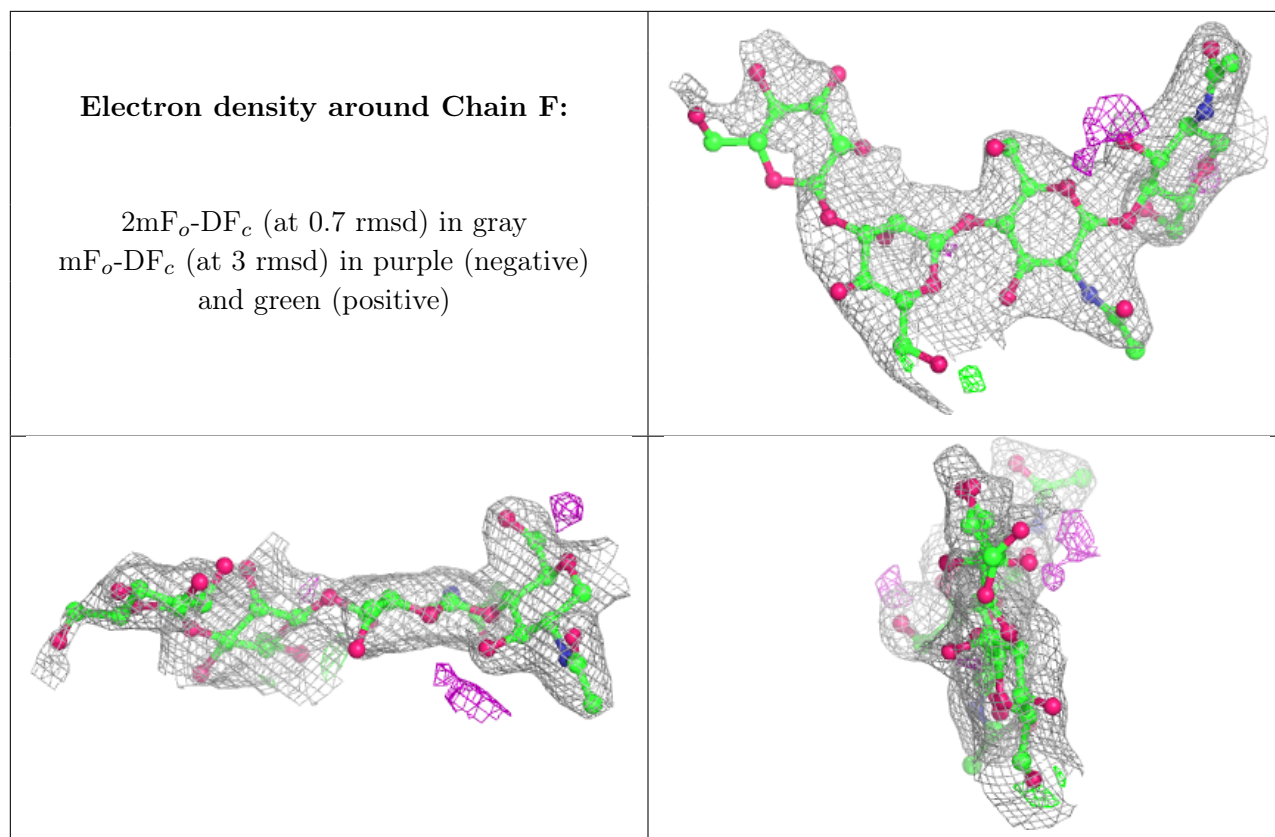
Electron density around Chain E:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around Chain H:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
10	MPD	X	101	8/8	0.78	0.12	83,87,91,91	0
11	ACT	A	928	4/4	0.83	0.14	74,85,87,88	0
10	MPD	X	103	8/8	0.88	0.21	82,89,94,96	0
10	MPD	A	925	8/8	0.89	0.17	50,56,61,64	0
10	MPD	A	926	8/8	0.90	0.21	66,71,83,89	0
10	MPD	A	927	8/8	0.95	0.14	44,45,49,50	0
10	MPD	X	102	8/8	0.96	0.12	49,52,53,54	0
9	G88	A	905	14/14	0.98	0.13	34,36,38,38	0
7	CL	A	903	1/1	0.99	0.16	35,35,35,35	0
8	CA	A	904	1/1	0.99	0.17	32,32,32,32	0
6	ZN	A	901	1/1	1.00	0.18	34,34,34,34	0
6	ZN	A	902	1/1	1.00	0.19	33,33,33,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.